



SEQUENCE LISTING

<110> Edwards, David L.
Hernstadt, Corinna
Wilcox, Edward R.
Wong, Siu-Yin

<120> Process for Altering the Host Range of Bacillus thuringiensis Toxins, and
Novel Toxins Produced Thereby

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<140> US 10/035,060

<141> 2001-12-27

<150> US 09/405,788

<151> 1999-09-27

<150> US 08/855,160

<151> 1997-05-13

<150> US 08/580,781

<151> 1995-12-29

<150> US 08/420,615

<151> 1995-04-10

<150> US 08/097,808

<151> 1993-07-27

<150> US 07/980,128

<151> 1992-11-23

<150> US 07/803,920

<151> 1991-12-06

<150> US 07/356,599

<151> 1989-05-24

<150> US 06/904,572

<151> 1986-09-05

<150> US 06/808,129

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OCT 10 2002

TECH CENTER 1600/2900

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 Gly Tyr Ile Glu Val Pro Ile His Phe Pro Ser Thr Ser Thr Arg Tyr
 515 520 525
 Arg Val Arg Val Arg Tyr Ala Ser Val Thr Pro Ile His Leu Asn Val
 530 535 540
 Asn Trp Gly Asn Ser Ser Ile Phe Ser Asn Thr Val Pro Ala Thr Ala
 545 550 555 560
 Thr Ser Leu Asp Asn Leu Gln Ser Ser Asp Phe Gly Tyr Phe Glu Ser
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 Ala Asn Ala Phe Thr Ser Ser Leu Gly Asn Ile Val Gly Val Arg Asn
 580 585 590
 Phe Ser Gly Thr Ala Gly Val Ile Ile Asp Arg Phe Glu Phe Ile Pro
 595 600 605
 Val Thr Ala Thr Leu Glu Ala Glu Tyr Asn Leu Glu Arg Ala Gln Lys
 610 615 620
 Ala Val Asn Ala Leu Phe Thr Ser Thr Asn Gln Leu Gly Leu Lys Thr
 625 630 635 640
 Asn Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Thr Tyr
 645 650 655
 Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys
 660 665 670
 Val Lys His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp
 675 680 685
 Ser Asn Phe Lys Asp Ile Asn Arg Gln Pro Glu Arg Gly Trp Gly Gly
 690 695 700
 Ser Thr Gly Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn
 705 710 715 720
 Tyr Val Thr Leu Ser Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu
 725 730 735
 Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Phe Thr Arg Tyr Gln
 740 745 750
 Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile
 755 760 765

Arg Tyr Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser
 770 775 780
 Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro
 785 790 795 800
 Asn Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser
 805 810 815
 Cys Arg Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu
 820 825 830
 Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp
 835 840 845
 Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn
 850 855 860
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 Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu
 885 890 895
 Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala
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 Leu Phe Val Asn Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr Asn Ile
 915 920 925
 Ala Met Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala
 930 935 940
 Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe
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 Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp
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 995 1000 1005
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 Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu
 1040 1045 1050
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 1055 1060 1065

Ile Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Val Asn
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 1085 1090 1095
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 1100 1105 1110
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 1115 1120 1125
 Asn Arg Gly Tyr Arg Asp Tyr Thr Pro Leu Pro Val Gly Tyr Val
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 <213> Bacillus thuringiensis

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 gttgatataa tatggggaat ttttggtccc tctcaatggg acgcatttct tgtacaaatt 240
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<210> 6

<211> 1177

<212> PRT

<213> Bacillus thuringiensis

<400> 6

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Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
35 40 45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
50 55 60

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
65 70 75 80

Glu	Gln	Leu	Ile	Asn	Gln	Arg	Ile	Glu	Glu	Phe	Ala	Arg	Asn	Gln	Ala	85	90	95
Ile	Ser	Arg	Leu	Glu	Gly	Leu	Ser	Asn	Leu	Tyr	Gln	Ile	Tyr	Ala	Glu	100	105	110
Ser	Phe	Arg	Glu	Trp	Glu	Ala	Asp	Pro	Thr	Asn	Pro	Ala	Leu	Arg	Glu	115	120	125
Glu	Met	Arg	Ile	Gln	Phe	Asn	Asp	Met	Asn	Ser	Ala	Leu	Thr	Thr	Ala	130	135	140
Ile	Pro	Leu	Phe	Ala	Val	Gln	Asn	Tyr	Gln	Val	Pro	Leu	Leu	Ser	Val	145	150	155
Tyr	Val	Gln	Ala	Ala	Asn	Leu	His	Leu	Ser	Val	Leu	Arg	Asp	Val	Ser	165	170	175
Val	Phe	Gly	Gln	Arg	Trp	Gly	Phe	Asp	Ala	Ala	Thr	Ile	Asn	Ser	Arg	180	185	190
Tyr	Asn	Asp	Leu	Thr	Arg	Leu	Ile	Gly	Asn	Tyr	Thr	Asp	Tyr	Ala	Val	195	200	205
Arg	Trp	Tyr	Asn	Thr	Gly	Leu	Glu	Arg	Val	Trp	Gly	Pro	Asp	Ser	Arg	210	215	220
Asp	Trp	Val	Arg	Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Leu	Thr	Leu	Thr	Val	225	230	235
Leu	Asp	Ile	Val	Ala	Leu	Phe	Pro	Asn	Tyr	Asp	Ser	Arg	Arg	Tyr	Pro	245	250	255
Ile	Arg	Thr	Val	Ser	Gln	Leu	Thr	Arg	Glu	Ile	Tyr	Thr	Asn	Pro	Val	260	265	270
Leu	Glu	Asn	Phe	Asp	Gly	Ser	Phe	Arg	Gly	Ser	Ala	Gln	Gly	Ile	Glu	275	280	285
Arg	Ser	Ile	Arg	Ser	Pro	His	Leu	Met	Asp	Ile	Leu	Asn	Ser	Ile	Thr	290	295	300
Ile	Tyr	Thr	Asp	Ala	His	Arg	Gly	Tyr	Tyr	Tyr	Trp	Ser	Gly	His	Gln	305	310	315
Ile	Met	Ala	Ser	Pro	Val	Gly	Phe	Ser	Gly	Pro	Glu	Phe	Thr	Phe	Pro	325	330	335
Leu	Tyr	Gly	Thr	Met	Gly	Asn	Ala	Ala	Pro	Gln	Gln	Arg	Ile	Val	Ala	340	345	350
Gln	Leu	Gly	Gln	Gly	Val	Tyr	Arg	Thr	Leu	Ser	Ser	Thr	Leu	Tyr	Arg	355	360	365
Arg	Pro	Phe	Asn	Ile	Gly	Ile	Asn	Asn	Gln	Gln	Leu	Ser	Val	Leu	Asp	370	375	380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
 385 390 395 400
 Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asn Glu Ile Pro Pro Gln
 405 410 415
 Asn Asn Asn Val Pro Pro Arg Gln Glu Phe Ser His Arg Leu Ser His
 420 425 430
 Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
 435 440 445
 Arg Ala Pro Thr Phe Ser Trp Gln His Arg Ser Ala Glu Phe Asn Asn
 450 455 460
 Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr
 465 470 475 480
 Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly
 485 490 495
 Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg
 500 505 510
 Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg
 515 520 525
 Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg
 530 535 540
 Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn
 545 550 555 560
 Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn
 565 570 575
 Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn
 580 585 590
 Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu
 595 600 605
 Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val
 610 615 620
 Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val
 625 630 635 640
 Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser
 645 650 655
 Asp Glu Phe Cys Leu Asp Glu Lys Gln Glu Leu Ser Glu Lys Val Lys
 660 665 670
 His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn
 675 680 685

Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr
 690 695 700
 Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
 705 710 715 720
 Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
 725 730 735
 Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
 740 745 750
 Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
 755 760 765
 Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp
 770 775 780
 Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg
 785 790 795 800
 Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg
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 Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile
 820 825 830
 Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile
 835 840 845
 Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu
 850 855 860
 Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys
 865 870 875 880
 Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu
 885 890 895
 Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe
 900 905 910
 Val Asn Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr Asn Ile Ala Met
 915 920 925
 Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu
 930 935 940
 Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu
 945 950 955 960
 Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn
 965 970 975
 Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val
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Lys Gly His Val Asp Val Glu Glu Gln Asn Asn Gln Arg Ser Val Leu
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Val Leu Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val
 1010 1015 1020

Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu
 1025 1030 1035

Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn
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Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Ile Tyr
 1055 1060 1065

Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Val Asn Gln Glu
 1070 1075 1080

Glu Tyr Gly Gly Ala Tyr Thr Ser Arg Asn Arg Gly Tyr Asn Glu
 1085 1090 1095

Ala Pro Ser Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys
 1100 1105 1110

Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys Glu Phe Asn Arg
 1115 1120 1125

Gly Tyr Arg Asp Tyr Thr Pro Leu Pro Val Gly Tyr Val Thr Lys
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Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile
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Leu Met Glu Glu
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<211> 3531

<212> DNA

<213> Bacillus thuringiensis

<400> 7

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<210> 8

<211> 1177

<212> PRT

<213> *Bacillus thuringiensis*

<400> 8

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 Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
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 Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
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 Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
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 Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
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 Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
 100 105 110
 Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
 115 120 125
 Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
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 Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
 145 150 155 160
 Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
 165 170 175
 Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
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 Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
 195 200 205
 Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
 210 215 220
 Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
 225 230 235 240
 Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
 245 250 255
 Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
 260 265 270
 Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
 275 280 285
 Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
 290 295 300

Ile Tyr Thr Asp Ala His Lys Gly Glu Tyr Tyr Trp Ser Gly His Gln
 305 310 315 320
 Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
 325 330 335
 Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
 340 345 350
 Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
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 Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
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 Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
 385 390 395 400
 Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
 405 410 415
 Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
 420 425 430
 Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
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 Arg Ala Pro Thr Phe Ser Trp Gln His Arg Ser Ala Glu Phe Asn Asn
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 Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr
 465 470 475 480
 Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly
 485 490 495
 Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg
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 Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg
 515 520 525
 Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg
 530 535 540
 Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn
 545 550 555 560
 Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn
 565 570 575
 Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn
 580 585 590
 Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu
 595 600 605

Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val
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 Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val
 625 630 635 640
 Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser
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 Asp Glu Phe Cys Leu Asp Glu Lys Gln Glu Leu Ser Glu Lys Val Lys
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 His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn
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 Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr
 690 695 700
 Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
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 Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
 725 730 735
 Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
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 Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
 755 760 765
 Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp
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 Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg
 785 790 795 800
 Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg
 805 810 815
 Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile
 820 825 830
 Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile
 835 840 845
 Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu
 850 855 860
 Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys
 865 870 875 880
 Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu
 885 890 895
 Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe
 900 905 910

Val Asn Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr Asn Ile Ala Met
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 Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu
 930 935 940
 Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu
 945 950 955 960
 Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn
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 Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val
 980 985 990
 Lys Gly His Val Asp Val Glu Glu Gln Asn Asn Gln Arg Ser Val Leu
 995 1000 1005
 Val Leu Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val
 1010 1015 1020
 Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu
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 Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn
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 Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Ile Tyr
 1055 1060 1065
 Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Val Asn Gln Glu
 1070 1075 1080
 Glu Tyr Gly Gly Ala Tyr Thr Ser Arg Asn Arg Gly Tyr Asn Glu
 1085 1090 1095
 Ala Pro Ser Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys
 1100 1105 1110
 Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys Glu Phe Asn Arg
 1115 1120 1125
 Gly Tyr Arg Asp Tyr Thr Pro Leu Pro Val Gly Tyr Val Thr Lys
 1130 1135 1140
 Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile
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 Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu
 1160 1165 1170
 Leu Met Glu Glu
 1175

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<213> Artificial Sequence

<220>

<223> synthetic DNA fragment used to insert point mutations into
pEW3 to create the plasmid pACB-1.

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gcccccgagg caagaattta gtcatcgatt aagccatggt tcaatgttta gatctggctt 120
tagtaatagt agtgtaagta taataagagc t 151